

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2002, 16:39:25 : Search time 231.5 Seconds
(without alignment)
14834.978 Million cell updates/sec

Title: US-10-025-514-7
Perfect score: 1525
Sequence: 1 tctagaccatgtctggaag.....ccaactcagaagtagtcgac 1525

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	1525	100.0	1525	24	ABK88022
2	1196	78.4	1756	24	ABK88023
3	1194.8	78.3	1582	24	ABK88024
4	1191.6	78.1	1525	24	ABK88025
5	1191.4	78.1	1582	24	ABK88027
6	1191.4	78.1	1756	24	ABK88026
7	1182	77.5	1182	24	ABK88015
8	629.4	41.3	1260	19	AAV41730
9	436.4	28.6	1312	16	AAQ89254
Human alpha-1-try					

10	436.4	28.6	1312	19	AAV28471	Nucleotide sequenc
11	436.4	28.6	1312	21	AAZ90199	Human alpha-anti
12	433.4	28.4	1367	22	AA345052	cDNA encoding nove
13	433.2	28.4	1352	13	AAQ31403	Human alpha-1 anti
14	433.2	28.4	1352	24	ABL67511	Thyroid cancer rel
15	433.2	28.4	1371	24	ABK84495	Human cDNA differe
16	433.2	28.4	1371	24	ABL67510	Thyroid cancer rel
17	433.2	28.4	1433	10	AA91077	Sequence encoding
18	433.2	28.4	1434	5	AA40078	Sequence encoding
19	433.2	28.4	1434	20	AA383548	Human alpha-anti-
20	433.2	28.4	5932	21	AA245928	Nucleotide sequenc
21	433.2	28.4	6142	21	AA245932	Nucleotide sequenc
22	433.2	28.4	6142	21	AA245933	Nucleotide sequenc
23	433.2	28.4	6565	21	AA245935	Nucleotide sequenc
24	433.2	28.4	6714	21	AA245930	Nucleotide sequenc
25	433.2	28.4	6924	21	AA245934	Nucleotide sequenc
26	433.2	28.4	6924	21	AA245935	Nucleotide sequenc
27	433.2	28.4	6981	21	AA245931	Nucleotide sequenc
28	433.2	28.4	7054	21	AA245927	Nucleotide sequenc
29	432.8	28.4	7405	21	AA245926	Nucleotide sequenc
30	431.6	28.3	1352	18	AA72858	Nucleotide sequenc
31	430.4	28.2	1185	19	AAV41726	Human alpha-1-anti
32	430	28.2	1434	10	AA90341	Native coding sequ
33	429.6	28.2	1312	10	AA97127	Sequence of alpha-
34	429	28.1	1189	13	AAQ21125	Alpha-1-antitrypsi
35	428.4	28.1	1378	13	AAQ23746	Entire sequence of
36	428.4	28.1	1396	11	AAQ03184	Human alpha 1-anti
37	426.8	28.0	1185	7	AA60417	Sequence encoding
38	426.8	28.0	1423	6	AA50540	Sequence of human
39	425.2	27.9	1299	6	AA50540	Sequence encoding
40	425.2	27.9	1378	6	AA50021	Sequence of fusion
41	411.2	27.0	1390	22	AAH23089	Osteoarthritis tis
42	401.4	26.3	2013	24	ABL59152	Protease inhibitor
43	375.6	24.6	1242	18	AA79493	Recombinant squirr
44	362.8	23.8	1242	18	AA78180	Alpha-1-antitrypsi
45	360.8	23.7	1312	10	AA91078	

ALIGNMENTS

RESULT 1
ABK88022
ID ABK88022 standard; DNA; 1525 BP.
XX
AC ABK88022;
XX
DT 07-OCT-2002 (first entry)
XX
DE DNA sequence encoding SLAP1 fusion protein.
XX
DE Yeast; alpha factor; gene; ds; Alzheimer's disease; SLAP1;
KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;
KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;
KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;
KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
KW tumour metastasis; tumour angiogenesis; osteoporosis; Paget's disease;
KW glomerulonephritis; scleroderma; hypertension.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT RBS 6..8
FT /tag= a
FT /standard_name= "Ribosome binding site"
FT CDS 9..1520
FT /tag= b
FT /product= "SLAP1 fusion protein"
FT /misc_feature 12..332
FT /tag= c
FT /note= "SLP1 coding region"
FT misc_feature 333-335

FT misc_feature /tag= d
 FT 336..1517 /note= "linking codon"
 FT /tag= e
 FT /note= "AAT coding region"

WO200250287-A2.

27-JUN-2002.

18-DEC-2001; 2001WO-US49256.

18-DEC-2000; 2000US-256699P.

20-NOV-2001; 2001US-331966P.

(ARRI-) ARRIVA PHARM INC.

Barr FJ, Gibson HL, Pemberton P;

WPI; 2002-500631/53.

P-PSDB; AAU99881.

Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease inhibitor -

Example 1; Page 73-73; 134pp; English.

This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alpha-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active portion. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, otitis externa or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema and psoriasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour metastasis and tumour angiogenesis, gastric ulceration, osteoporosis, Paget's disease, glomerulonephritis, scleroderma, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the DNA encoding the SIAP1 fusion protein of the invention.

Sequence 1525 BP; 467 A; 286 C; 314 G; 458 T; 0 other;

Query Match 100.0%; Score 1525; DB 24; Length 1525;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAGACCATGCTGGAAGTCTTTCAAGCCCGGTGTGTCTCCACCAAGAGAGTCCGCTC 60
 DB 1 TCTAGACCATGCTGGAAGTCTTTCAAGCCCGGTGTGTCTCCACCAAGAGAGTCCGCTC 60
 QY 61 AATGTTTGAGATACAAGAGCCAGAAATGTCAATCCGACTGGCAATGTCCAGGTAAGAAGA 120
 DB 61 AATGTTTGAGATACAAGAGCCAGAAATGTCAATCCGACTGGCAATGTCCAGGTAAGAAGA 120
 QY 121 GATGTTGTCCAGACACTTGTGGTATCAAGTGTCTAGACCAGTGTGACACCCCAACCCCA 180
 DB 121 GATGTTGTCCAGACACTTGTGGTATCAAGTGTCTAGACCAGTGTGACACCCCAACCCCA 180
 QY 181 CTAGAAGAACCCAGGTAAGTGTCCAGTACTTACGGTCAATGTTGATGTTGAACCCAC 240
 DB 181 CTAGAAGAACCCAGGTAAGTGTCCAGTACTTACGGTCAATGTTGATGTTGAACCCAC 240
 QY 241 CAAACTCTGTGAATGACCGGTCAATGTATAGAGAGACTTGAAGTGTGTATGGGTATGT 300
 DB 241 CAAACTCTGTGAATGACCGGTCAATGTATAGAGAGACTTGAAGTGTGTATGGGTATGT 300

Db 241 CAAACTCTGTGAATGACCGGTCAATGTATAGAGAGACTTGAAGTGTGTATGGGTATGT 300
 QY 301 GTGGTAAGTCTGTGTTCCTCCAGTCAAGGCGCATGGAAGACCTTCAAGCGCAGCGCGCTC 360
 Db 301 GTGGTAAGTCTGTGTTCCTCCAGTCAAGGCGCATGGAAGACCTTCAAGCGCAGCGCGCTC 360
 QY 361 AAAAAACCGACACCATGATCATACGACCAAGACCATCCGACTTTTAAATAAAATTAATCTCAA 420
 Db 361 AAAAAACCGACACCATGATCATACGACCAAGACCATCCGACTTTTAAATAAAATTAATCTCAA 420
 QY 421 ATTTAGCCGAATTTGCTTTTCTTTGATAGACAATTAGCTCATCAAAAGTAATTTCTACTA 480
 Db 421 ATTTAGCCGAATTTGCTTTTCTTTGATAGACAATTAGCTCATCAAAAGTAATTTCTACTA 480
 QY 481 ACATTTTCTTTAGTCTGCTTTCTATTGCGCACTGCTTTGCGCCATGTTGAGTTAGTACTA 540
 Db 481 ACATTTTCTTTAGTCTGCTTTCTATTGCGCACTGCTTTGCGCCATGTTGAGTTAGTACTA 540
 QY 541 AAGCCGATACCCATGACGAGATTTTGAAGGTTTAAACTTTTAAATTTGACCGGAATCCCGAG 600
 Db 541 AAGCCGATACCCATGACGAGATTTTGAAGGTTTAAACTTTTAAATTTGACCGGAATCCCGAG 600
 QY 601 AAGCCCAATTCAGGAGGTTTTCAGAGTGTGTGAGAACTTTGAATCAACCTGATTTCTC 660
 Db 601 AAGCCCAATTCAGGAGGTTTTCAGAGTGTGTGAGAACTTTGAATCAACCTGATTTCTC 660
 QY 661 AATTGCAATTAACCTACTGCTAAGCGTTTATTTTGTCTGAAAGGTTTAAATTTGAGTGA 720
 Db 661 AATTGCAATTAACCTACTGCTAAGCGTTTATTTTGTCTGAAAGGTTTAAATTTGAGTGA 720
 QY 721 AATTCTTAGAAGCGTCAAGAACTATATCATAGTACGAGGCTTTTACCGTTAAATTTGGTG 780
 Db 721 AATTCTTAGAAGCGTCAAGAACTATATCATAGTACGAGGCTTTTACCGTTAAATTTGGTG 780
 QY 781 ATACTGAGGAGCTTAAAGCAAAATTAATGATTTGAGAAAGGACCCAGGGAAGA 840
 Db 781 ATACTGAGGAGCTTAAAGCAAAATTAATGATTTGAGAAAGGACCCAGGGAAGA 840
 QY 841 TCGTTGACCTAGTTTAAAGAAATTAGATCGTATACCGTCTTCGACACTAGTTAACTATATT 900
 Db 841 TCGTTGACCTAGTTTAAAGAAATTAGATCGTATACCGTCTTCGACACTAGTTAACTATATT 900
 QY 901 TTTTCAAGGTTAAGTGGGAGCGTCTTTCGAGGTTAAAGATACCTGAAGAGAGAGATTTTC 960
 Db 901 TTTTCAAGGTTAAGTGGGAGCGTCTTTCGAGGTTAAAGATACCTGAAGAGAGAGATTTTC 960
 QY 961 ATGTTGATCAAGTTACTACTGTCAAAAGTTCCAATGATGAAAGAGCTGGGTATGTTCAATA 1020
 Db 961 ATGTTGATCAAGTTACTACTGTCAAAAGTTCCAATGATGAAAGAGCTGGGTATGTTCAATA 1020
 QY 1021 TTCAACATTTGCAAAATAATTAAGTTCTTGGGTCTTATTAATCAAGTATTTAGGTAAACGCTA 1080
 Db 1021 TTCAACATTTGCAAAATAATTAAGTTCTTGGGTCTTATTAATCAAGTATTTAGGTAAACGCTA 1080
 QY 1081 CTGCTATTTTCTTACCGAGAGGTAAGCTTCAACATTTAGAGAAATGAGTTGACTC 1140
 Db 1081 CTGCTATTTTCTTACCGAGAGGTAAGCTTCAACATTTAGAGAAATGAGTTGACTC 1140
 QY 1141 ATGACATATTTACTAAATTTTATAGAGAACGAGGATCGTCTGAGCCCTCTCTGACCTGTC 1200
 Db 1141 ATGACATATTTACTAAATTTTATAGAGAACGAGGATCGTCTGAGCCCTCTCTGACCTGTC 1200
 QY 1201 CAAAGTTAAGTATACCGGTACTTACGACTTAAATCTGTTTAGCCAGTTAGGTATTA 1260
 Db 1201 CAAAGTTAAGTATACCGGTACTTACGACTTAAATCTGTTTAGCCAGTTAGGTATTA 1260
 QY 1261 CCAAGTTTCTTACCGGTGCGGATTTGAGTGGTGTACTGAAGAGCTCCATTAAAT 1320
 Db 1261 CCAAGTTTCTTACCGGTGCGGATTTGAGTGGTGTACTGAAGAGCTCCATTAAAT 1320
 QY 1321 TGAGTAAAGCTGTTTCAAAAGCGCTCTTAACCTATTGATGAAAGGTTACCGAGCGCGCG 1380
 Db 1321 TGAGTAAAGCTGTTTCAAAAGCGCTCTTAACCTATTGATGAAAGGTTACCGAGCGCGCG 1380


```

Db 1221 CCAATGATGAAAGACTGGGTATGTTCAATATTCACATTCGAAAAATTAAGTCTTGG 1280
QY 1050 GTCTTATTAATGAAGTATTTAGGTAAAGCTACTGCTATTTTTCCTACGAGCAAGGT 1109
Db 1281 GTCTTATTAATGAAGTATTTAGGTAAAGCTACTGCTATTTTTCCTACGAGCAAGGT 1340
QY 1110 AAGCTTCAACATTTAGAGAATAGTGTGACTCATGACATTTACTAAATTTTTCAGAGAAC 1169
Db 1341 AAGCTTCAACATTTAGAGAATAGTGTGACTCATGACATTTACTAAATTTTTCAGAGAAC 1400
QY 1170 GAGATCGTGCAGCTCTCTGACCTGCCAAAGTTAAGTATATCACCAGTACTTACGAC 1229
Db 1401 GAGATCGTGCAGCTCTCTGACCTGCCAAAGTTAAGTATATCACCAGTACTTACGAC 1460
QY 1230 TAAATCTGTTTTCAGCCAGTTAGGTTATTAACCAAGTTTTCCTAACGGTCCGATTTG 1289
Db 1461 TTAATCTGTTTTCAGCCAGTTAGGTTATTAACCAAGTTTTCCTAACGGTCCGATTTG 1520
QY 1290 AGTGTGTTTACTGAAGAAGCTCCATTAATTTAGTAAAGCTGTTCACAAAGCCGCTTA 1349
Db 1521 AGTGTGTTTACTGAAGAAGCTCCATTAATTTAGTAAAGCTGTTCACAAAGCCGCTTA 1580
QY 1350 ACTATTGATGAAAGGTTACGAGCGCCGCGCTATGTTCTGGAAGCTATTCCAATG 1409
Db 1581 ACTATTGATGAAAGGTTACGAGCGCCGCGCTATGTTCTGGAAGCTATTCCAATG 1640
QY 1410 AGCATTCACCAAGATTAATTTAATAACCATTCGTTTCTGATGATCGAGCAAGAC 1469
Db 1641 AGCATTCACCAAGATTAATTTAATAACCATTCGTTTCTGATGATCGAGCAAGAC 1700
QY 1470 ACTAAAGCCCATGTTTATGGTGAAGTGTGTCACCAACTCAGAAAGTAGTCGAC 1525
Db 1701 ACTAAAGCCCATGTTTATGGTGAAGTGTGTCACCAACTCAGAAAGTAGTCGAC 1756

```

```

RESULT 3
ABK88024
ID ABK88024 standard; DNA; 1582 BP.
XX AC ABK88024;
XX DT 07-OCT-2002 (first entry)
XX DE DNA sequence encoding N-TAP1 fusion protein.
XX KW NTAP1; gene; ds; Alzheimer's disease; tumour angiogenesis;
XX KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;
XX KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;
XX KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;
XX KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
XX KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;
XX KW glomerulonephritis; hypertension.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key
XX FT RBS
XX FT Location/Qualifiers
XX FT 6..8
XX FT /*tag= a
XX FT /standard_name= "Ribosome binding site"
XX FT 9..1577
XX FT /*tag= b
XX FT /product= "NTAP1 fusion protein"
XX FT 12..389
XX FT /*tag= c
XX FT /note= "TIMP-1 coding region"
XX FT 390..392
XX FT /*tag= d
XX FT /note= "linking codon"
XX FT 393..1574
XX FT /*tag= e
XX FT /note= "AAT coding region"
XX FT

```

```

XX WO200250287-A2.
XX PD 27-JUN-2002.
XX PF 18-DEC-2001; 2001WO-US49256.
XX PR 18-DEC-2000; 2000US-256699P.
XX PR 20-NOV-2001; 2001US-331966P.
XX PA (ARRI-) ARRIVA PHARM INC.
XX PI Barr PJ, Gibson HL, Pemberton P;
XX DR WPI; 2002-500631/53.
XX DR P-PSDB; AAU99883.
XX PS Novel fusion protein useful for inhibiting protease activity associated
XX with a disorder such as emphysema, asthma, comprises a first protease
XX inhibitor comprising alpha 1-antitrypsin and a second protease
XX inhibitor -
XX Example 2; Page 85-86; 134pp; English.
XX This invention relates to a novel fusion protein comprising a first
XX protease inhibitor comprising an alpha 1-antitrypsin or its functionally
XX active portion and a second protease inhibitor or its functionally
XX active portion. The fusion proteins of the invention may act as an
XX inhibitor of protease activity. The fusion protein of the invention
XX is useful for inhibiting protease activity associated with a disorder
XX such as emphysema, asthma, chronic obstructive pulmonary disease,
XX cystic fibrosis, otitis media, otitis externa or HIV infection, or
XX for treating an individual suffering from or at risk for a disease or
XX disorder involving unwanted protease activity. The proteins are useful
XX for treating dermatological diseases such as atopic dermatitis, eczema
XX and psoriasis, in inflammatory responses to viral infection, and for
XX treating herpes infection, corneal or epidermal ulceration, chronic
XX non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,
XX tumour metastasis and tumour angiogenesis, gastric ulceration,
XX osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,
XX bacterial infection, Alzheimer's disease, hypertension and muscular
XX dystrophy. The present sequence represents the DNA encoding the
XX NTAP1 fusion protein of the invention.
XX SQ Sequence 1582 BP; 464 A; 333 C; 329 G; 456 T; 0 other;
XX
XX Query Match 78.3%; Score 1194.8; DB 24; Length 1582;
XX Best Local Similarity 99.8%; Pred. No. 2.7e-290;
XX Matches 1196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 328 AGGCATGGAAGACCCCTCAAGGCGCGCGCTCAAAAAACCGACACCATCATCAGGACC 387
Db 385 AGGAAATGGAAGACCCCTCAAGGCGCGCGCTCAAAAAACCGACACCATCATCAGGACC 444
QY 388 AAGACCATCCGACTTTTAAATAAATTAATCTCAAAATTTAGCCGAATTTGTTCTTCT 447
Db 445 AAGACCATCCGACTTTTAAATAAATTAATCTCAAAATTTAGCCGAATTTGTTCTTCT 504
QY 448 ATAGACAATTAGCTCATCAAGTAATTTCTACTACATTTTTCCTGCTCTTCTATTG 507
Db 505 ATAGACAATTAGCTCATCAAGTAATTTCTACTACATTTTTCCTGCTCTTCTATTG 564
QY 508 CCACTGCTTTCCGCTATGTTAGTTTACTAAAGCCGATACCCATGACGAGATTTTAG 567
Db 565 CCACTGCTTTCCGCTATGTTAGTTTACTAAAGCCGATACCCATGACGAGATTTTAG 624
QY 568 AAGGTTTAAACTTTAATTTGACCAGAAATCCAGAGCCCAAAATTCAGAGGGTTTCAAG 627
Db 625 AAGGTTTAAACTTTAATTTGACCAGAAATCCAGAGCCCAAAATTCAGAGGGTTTCAAG 684
QY 628 AGTTGTTGAGAACTTTGAATCAACTGATTTCTCAATTTGCAATTAACCTACTGTTA 687
Db 685 AGTTGTTGAGAACTTTGAATCAACTGATTTCTCAATTTGCAATTAACCTACTGTTA 744

```

QY 688 TATTTTCTGCTGAAGGTTTAAATTTGGTTCACAAATTCCTAGAGAGCGTCAAGAACTAT 747
KW |
XX |
DQ 745 TATTTTCTGCTGAAGGTTTAAATTTGGTTCACAAATTCCTAGAGAGCGTCAAGAACTAT 804
OS |
XX |
DQ 748 ATCATAGTGAAGGTTTACCGTTAAATTTGGTTCACAAATTCCTAGAGAGCGTCAAGAACTAT 807
OS |
XX |
DQ 805 ATCATAGTGAAGGTTTACCGTTAAATTTGGTTCACAAATTCCTAGAGAGCGTCAAGAACTAT 864
OS |
XX |
DQ 808 ATCATAGTGAAGGTTTACCGTTAAATTTGGTTCACAAATTCCTAGAGAGCGTCAAGAACTAT 867
OS |
XX |
DQ 865 ATCATAGTGAAGGTTTACCGTTAAATTTGGTTCACAAATTCCTAGAGAGCGTCAAGAACTAT 924
OS |
XX |
DQ 868 GTGATACCGTCTTCGACACAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGTGAAGT 927
OS |
XX |
DQ 925 GTGATACCGTCTTCGACACAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGTGAAGT 984
OS |
XX |
DQ 928 TCGAGTTTAAAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGTGAAGT 987
OS |
XX |
DQ 985 TCGAGTTTAAAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGTGAAGT 1044
OS |
XX |
DQ 988 TCCCAATGATGAAGGAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1047
OS |
XX |
DQ 1045 TCCCAATGATGAAGGAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1104
OS |
XX |
DQ 1048 GGGTCTTATTAATGAAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1107
OS |
XX |
DQ 1105 GGGTCTTATTAATGAAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1164
OS |
XX |
DQ 1108 GTAGCTTCAACATTTAGAGATGAGTGAAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1167
OS |
XX |
DQ 1165 GTAGCTTCAACATTTAGAGATGAGTGAAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1224
OS |
XX |
DQ 1168 ACAGGATCGTGTGAGGAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1227
OS |
XX |
DQ 1225 ACAGGATCGTGTGAGGAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1284
OS |
XX |
DQ 1228 ACTTAAATCTGTTTACGACAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1287
OS |
XX |
DQ 1285 ACTTAAATCTGTTTACGACAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1344
OS |
XX |
DQ 1288 TGAGTGTGTTTACTGAAGAGTCCATTAATTTTGAAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1347
OS |
XX |
DQ 1345 TGAGTGTGTTTACTGAAGAGTCCATTAATTTTGAAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1404
OS |
XX |
DQ 1348 TAACATTTGATGAAGAGTACCGAGGAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1407
OS |
XX |
DQ 1405 TAACATTTGATGAAGAGTACCGAGGAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1464
OS |
XX |
DQ 1408 TGAGCATTTCCACAGAGTAAATTTTAAAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1467
OS |
XX |
DQ 1465 TGAGCATTTCCACAGAGTAAATTTTAAAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1524
OS |
XX |
DQ 1468 ACATTAAGGAGGAGTAACTGAGGAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1525
OS |
XX |
DQ 1525 ACATTAAGGAGGAGTAACTGAGGAGTAACTGAGGAGTAACTATATTTTTCAGGTTAAAGTGAAGTGAAGT 1582
OS |
XX |

RESULT 4

ABK88025

ID ABK88025 standard; DNA: 1525 BP.

AC ABK88025;

XX

XX

DT 07-OCT-2002 (first entry)

XX

XX

DE DNA sequence encoding rSLAP1 fusion protein.

KW rSLAP1; gene: ds; Alzheimer's disease; tumour angiogenesis;

KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;

KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;

KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;

KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;

KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;
XX glomerulonephritis; hypertension.
OS Homo sapiens.
XX Synthetic.
FH Key
FT RBS
FT Location/Qualifiers
FT 6..8
FT /tag= a
FT /standard_name= "Ribosome binding site"
FT 9..1520
FT /tag= b
FT /product= "rSLAP1 fusion protein"
FT 12..1193
FT /tag= c
FT /note= "AAT coding region"
FT 1194..1196
FT /tag= d
FT /note= "Linking codon"
FT 1197..1517
FT /tag= e
FT /note= "SLP1 coding region"
XX
XX WO200250287-A2.
XX
XX 27-JUN-2002.
XX
XX 18-DEC-2001; 2001WO-US49256.
XX
XX 18-DEC-2000; 2000US-256699P.
XX 20-NOV-2001; 2001US-331966P.
XX (ARRI-) ARRIVA PHARM INC.
XX
XX Barr PJ, Gibson HL, Pemberton P;
XX
XX WPI: 2002-500631/53.
XX P-PSDB: AAU99884.
XX
XX Novel fusion protein useful for inhibiting protease activity associated
XX with a disorder such as emphysema, asthma, comprises a first protease
XX inhibitor comprising alpha 1-antitrypsin and a second protease
XX inhibitor.
XX
XX Example 3; Page 89-90; 134pp; English.
XX
XX This invention relates to a novel fusion protein comprising a first
XX protease inhibitor comprising an alpha 1-antitrypsin or its functionally
XX active portion and a second protease inhibitor or its functionally
XX active portion. The fusion proteins of the invention may act as an
XX inhibitor of protease activity. The fusion protein of the invention
XX is useful for inhibiting protease activity associated with a disorder
XX such as emphysema, asthma, chronic obstructive pulmonary disease,
XX cystic fibrosis, otitis media, otitis externa or HIV infection, or
XX for treating an individual suffering from or at risk for a disease or
XX disorder involving unwanted protease activity. The proteins are useful
XX for treating dermatological diseases such as atopic dermatitis, eczema
XX and psoriasis, in inflammatory responses to viral infection, and for
XX treating herpes infection, corneal or epidermal ulceration, chronic
XX non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,
XX tumour metastasis and tumour angiogenesis, gastric ulceration,
XX osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,
XX bacterial infection, Alzheimer's disease, hypertension and muscular
XX dystrophy. The present sequence represents the DNA encoding the
XX rSLAP1 fusion protein of the invention.
XX
XX Sequence 1525 BP; 467 A; 287 C; 314 G; 457 T; 0 other;

Query Match

Best Local Similarity 78.1%; Score 1191.6; DB 24; Length 1525;

Matches 1194; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 325 TCAAGGCCATGGAAGACCTCAAGGCGCGCTCAAAAAACCCAGCAGTCATCAGC 384

Db	1081	CAATGAGCATCCACCAGAAAGTTAAATTAATAAACCAATTCGTTTCTGTATGATCGAGC	1140
QY	1465	AGAACACTAAAGCCCATTTGTTATGGGTAAAGTTGTCAACCCCACTCAGAAGTAGTC	1522
Db	1141	AGAACACTAAAGCCCATTTGTTATGGGTAAAGTTGTCAACCCCACTCAGAAGTAGTC	1198
RESULT 5			
ABK88027			
ID	ABK88027	standard; DNA; 1582 BP.	
XX			
AC	ABK88027;		
XX			
DT	07-OCT-2002	(first entry)	
XX			
DE	DNA sequence encoding rN-TAP1 fusion protein.		
XX			
KW	rN-TAP1; gene; ds; Alzheimer's disease; tumour angiogenesis;		
KW	malaria; emphysema; asthma; chronic obstructive pulmonary disease;		
KW	cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;		
KW	human immunodeficiency virus; atopic dermatitis; muscular dystrophy;		
KW	herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;		
KW	tumour metastasis; osteoporosis; Paget's disease; scleroderma;		
KW	glomerulonephritis; hypertension.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
PH	Key	Location/Qualifiers	
FT	RBS	6..8	
FT		/tag= a	
FT		/standard_name= "Ribosome binding site"	
FT	CDS	9..1577	
FT		/tag= b	
FT		/product= "rTAP1 fusion protein"	
FT	misc_feature	12..1193	
FT		/tag= c	
FT		/note= "AT coding region"	
FT	misc_feature	1194..1196	
FT		/tag= d	
FT		/note= "linking codon"	
FT	misc_feature	1197..1574	
FT		/tag= e	
FT		/note= "TIMP-1 coding region"	
XX			
PN	WO200250287-A2.		
XX			
PD	27-JUN-2002.		
XX			
PF	18-DEC-2001; 2001WO-US49256.		
XX			
PR	18-DEC-2000; 2000US-256699P.		
PR	20-NOV-2001; 2001US-331966P.		
XX			
PA	(ARRI-) ARRIVA PHARM INC.		
XX			
PI	Barr PJ, Gibson HL, Pemberton P;		
XX			
DR	WPI; 2002-500631/53.		
DR	P-PSDB; AAU99885.		
XX			
PT	Novel fusion protein useful for inhibiting protease activity associated		
PT	with a disorder such as emphysema, asthma, comprises a first protease		
PT	inhibitor comprising alpha 1-antitrypsin and a second protease		
PT	inhibitor		
XX			
PS	Example 3; Page 95-96; 134pp; English.		
XX			
CC	This invention relates to a novel fusion protein comprising a first		
CC	protease inhibitor comprising an alpha-antitrypsin or its functionally		
CC	active portion and a second protease inhibitor or its functionally		
CC	active protein. The fusion proteins of the invention may act as an		
CC	inhibitor of protease activity. The fusion protein of the invention		

27-JUN-2002.
 18-DEC-2001; 2001WO-US49256.
 18-DEC-2000; 2000US-256699P.
 20-NOV-2001; 2001US-331966P.
 (ARRI-) ARRIVA PHARM INC.
 Barr PJ, Gibson HL, Pemberton P;
 WPI; 2002-500631/53.
 P-PSDB; AAU99889.
 Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease inhibitor -
 Example 3; Page 92-93; 134pp; English.
 This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alpha1-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active portion. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, otitis externa or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema and psoriasis, in inflammatory responses to viral infection, chronic treating herpes infection, rheumatoid arthritis, periodontal disease, non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour metastasis and tumour angiogenesis, gastric ulceration, osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the DNA encoding the rTAP1 fusion protein of the invention.
 Sequence 1756 BP; 493 A; 394 C; 374 G; 495 T; 0 other;
 Query Match 78.1%; Score 1191.4; DB 24; Length 1756;
 Best Local Similarity 99.5%; Pred. No. 2e-289;
 Matches 1195; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 325 TCAAGGCCATGGAGACCCCTCAAGCGACGCGCTCAAAAACCCGACACCATCATCAGC 384
 1 TCTAGACCATGGAGACCCCTCAAGCGACGCGCTCAAAAACCCGACACCATCATCAGC 60
 365 ACCAAGACCATCCGACTTTTAAATAAAATTAATCTCAAAATTTAGCCGAATTTGCTTTTCT 444
 61 ACCAAGACCATCCGACTTTTAAATAAAATTAATCTCAAAATTTAGCCGAATTTGCTTTTCT 120
 445 TGTATAGACAATAGCTCATCAAGTAATCTACTACATTTTCTTACTGCTGTTCTCA 504
 121 TGTATAGACAATAGCTCATCAAGTAATCTACTACATTTTCTTACTGCTGTTCTCA 180
 505 TTGCCACTGCTTTGCCCATGTTGAGTTTAGGTACTAAAGCCGATACCATGACGAGATTT 564
 181 TTGCCACTGCTTTGCCCATGTTGAGTTTAGGTACTAAAGCCGATACCATGACGAGATTT 240
 565 TAGAAGGTTTAAACTTTAATTTAGCCGAATTTAGCCGAATTTAGCCGAATTTAGCCGAATTT 624
 241 TAGAAGGTTTAAACTTTAATTTAGCCGAATTTAGCCGAATTTAGCCGAATTTAGCCGAATTT 300
 625 AGAGTTGTTAGAACTTTGATCAACCTGATCTCAATTCGAATTAACCTACTGTTAAGC 684
 301 AGAGTTGTTAGAACTTTGATCAACCTGATCTCAATTCGAATTAACCTACTGTTAAGC 360
 685 GTTTATTTTGTCTGAAGGTTTAAATTTAGGTTGACAAATTTCTTGAAGACGCTGAAGAAC 744

Db 361 GTTATTTTGTCTGAAGGTTTAAATTTGTTTACAAATTTCTTGAAGACGTTCAAGAAC 420
 Qy 745 TATATCATAGTGAAGGCTTTTACCGTTAAATTTGGTGATGATGAGGAGCTAAAGACAAA 804
 Db 421 TATATCATAGTGAAGGCTTTTACCGTTAAATTTGGTGATGATGAGGAGCTAAAGACAAA 480
 Qy 805 TTAATGATTTATGTTGAGAAAGGACCCAGGTAAGATCGTTGACCTAGTTAAAGAAATTAG 864
 Db 481 TTAATGATTTATGTTGAGAAAGGACCCAGGTAAGATCGTTGACCTAGTTAAAGAAATTAG 540
 Qy 865 ATCGTGATACCGTCTTCCGCACTAGTTAACTATATATTTTTCAGGGTAAGTGGGAACGTC 924
 Db 541 ATCGTGATACCGTCTTCCGCACTAGTTAACTATATATTTTTCAGGGTAAGTGGGAACGTC 600
 Qy 925 CTTTCGAGGTTTAAAGATGATGAGGAGGAGATTTTCATGTTGATCAAGTTACTACTGTTCA 984
 Db 601 CTTTCGAGGTTTAAAGATGATGAGGAGGAGATTTTCATGTTGATCAAGTTACTACTGTTCA 660
 Qy 985 AAGTTCGAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1044
 Db 661 AAGTTCGAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
 Qy 1045 CTTTCGAGGTTTAAAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1104
 Db 721 CTTTCGAGGTTTAAAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
 Qy 1105 AAGTTCGAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1164
 Db 781 AAGTTCGAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
 Qy 1165 AGAACGAGGATGCTGCTGAGCGCTTCTCTGACCTGCCAAAGTTAAGTATACCGGCTACTT 1224
 Db 841 AGAACGAGGATGCTGCTGAGCGCTTCTCTGACCTGCCAAAGTTAAGTATACCGGCTACTT 900
 Qy 1225 ACAGCTTAAATCTGTTTGGCCAGTTAGGTTATACCAAGTTTCTTCTGAGGAGGAGGAGG 1284
 Db 901 ACAGCTTAAATCTGTTTGGCCAGTTAGGTTATACCAAGTTTCTTCTGAGGAGGAGGAGG 960
 Qy 1285 ATTTGAGTGGTGTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1344
 Db 961 ATTTGAGTGGTGTACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
 Qy 1345 TCTTAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1404
 Db 1021 TCTTAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
 Qy 1405 CAATGACATTCACCCAGAGTTTAAATTTAAATAAACCATTCGTTTCTGATGATGAGGAGG 1464
 Db 1081 CAATGACATTCACCCAGAGTTTAAATTTAAATAAACCATTCGTTTCTGATGATGAGGAGG 1140
 Qy 1465 AGAACATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1524
 Db 1141 AGAACATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
 Qy 1525 C 1525
 Db 1201 C 1201
 RESULT 7
 ABK88015
 ID ABK88015 standard; DNA; 1182 BP.
 XX
 AC ABK88015;
 DX
 DT 07-OCT-2002 (first entry)
 XX
 DE DNA encoding human alpha-1-antitrypsin (AAT) protein.
 XX Alpha-1-antitrypsin; AAT: human; gene; ds; protease inhibitor; malaria;
 KW emphysema; asthma; chronic obstructive pulmonary disease; eczema;
 KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis;
 KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;

KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
 KW tumour metastasis; tumour angiogenesis; osteoporosis; Paget's disease;
 KW glomerulonephritis; scleroderma; Alzheimer's disease; hypertension.
 OS Homo sapiens.

XX FH	Key	Location/Qualifiers
XX FT	CDS	1..1182
XX FT	/tag=	a
XX FT	/product=	"Alpha-1-antitrypsin"
XX FT	/partial	
XX FT	/note=	"No start or stop codon shown"

W0200250287-A2.

XX XX

PD 27-JUN-2002.

XX XX

PF 18-DEC-2001; 2001WO-US49256.

XX XX

PR 18-DEC-2000; 2000US-256699P.

XX XX

PR 20-NOV-2001; 2001US-331966P.

XX XX

PA (ARRI-) ARRIVA PHARM INC.

XX XX

PI Barr PJ, Gibson HL, Pemberton P;

XX XX

DR WPI; 2002-500631/53.

XX XX

DR P-PSDB; AAU99873.

XX XX

PT Novel fusion protein useful for inhibiting protease activity associated
 with a disorder such as emphysema, asthma, comprises a first protease
 PT inhibitor comprising alpha 1-antitrypsin and a second protease
 PT inhibitor -

XX XX

PS Disclosure; Page 24-25; 134pp; English.

XX XX

CC This invention relates to a novel fusion protein comprising a first
 CC protease inhibitor comprising an alpha1-antitrypsin or its functionally
 CC active portion and a second protease inhibitor or its functionally
 CC active protein. The fusion proteins of the invention may act as an
 CC inhibitor of protease activity. The fusion protein of the invention
 CC is useful for inhibiting protease activity associated with a disorder
 CC such as emphysema, asthma, chronic obstructive pulmonary disease,
 CC cystic fibrosis, otitis media, otitis externa or HIV infection, or
 CC for treating an individual suffering from or at risk for a disease or
 CC disorder involving unwanted protease activity. The proteins are useful
 CC for treating dermatological diseases such as atopic dermatitis, eczema
 CC and psoriasis, in inflammatory responses to viral infection, and for
 CC treating herpes infection, corneal or epidermal ulceration, chronic
 CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,
 CC tumour metastasis and tumour angiogenesis, gastric ulceration,
 CC osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,
 CC bacterial infection, Alzheimer's disease, hypertension and muscular
 CC dystrophy. The present sequence represents the DNA encoding the human
 CC alpha-1-antitrypsin (AAT) protein used to create the fusion protein
 CC of the invention.

XX XX

SQ Sequence 1182 BP; 369 A; 214 C; 229 G; 370 T; 0 other;

Query Match 77.5%; Score 1182; DB 24; Length 1182;
 Best Local Similarity 100.0%; Pred. No. 4e-287;
 Matches 1182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	336	GAAGACCTCAAGCGACGCGCTCAAAAACCGACACGAGTCATCACGACCAAGACCAT	395
Db	1	GAAGACCTCAAGCGACGCGCTCAAAAACCGACACGAGTCATCACGACCAAGACCAT	60
Qy	396	CCGACTTTTAAATAAATTAATCAATTTAGCGGAATTTGCTTTTCTTTGTATAGACAA	455
Db	61	CCGACTTTTAAATAAATTAATCAATTTAGCGGAATTTGCTTTTCTTTGTATAGACAA	120
Qy	456	TTAGCTCATCAAGTAATTTCTACTAATTTTTTTTAGTCCTGTTTCTTATGCCACTGCT	515

Db	121	TTAGCTCATCAAGTAATTTCTACTAATTTTTTTTAGTCCTGTTTCTTATGCCACTGCT	180
Qy	516	TTGCGCCATGTTGAGTTTAGGTACTAAGCCGATACCCATGACGAGATTTTGAAGGTTTA	575
Db	181	TTGCGCCATGTTGAGTTTAGGTACTAAGCCGATACCCATGACGAGATTTTGAAGGTTTA	240
Qy	576	AACTTTAAATTTGACCGAAATCCAGAGCCCAAAATTCACGAGGGTTTTCAGAGAGTTGTTG	635
Db	241	AACTTTAAATTTGACCGAAATCCAGAGCCCAAAATTCACGAGGGTTTTCAGAGAGTTGTTG	300
Qy	636	AGAACTTTGAATCAACCTGATTCCTCAATTTGCAATTAAGTAACTACTGTTAACTGTTT	695
Db	301	AGAACTTTGAATCAACCTGATTCCTCAATTTGCAATTAAGTAACTACTGTTAACTGTTT	360
Qy	696	TCTGAAGGTTTAAATTTGTTGACAAATTCCTAGAAGACGTCAGAACTATATCATAGT	755
Db	361	TCTGAAGGTTTAAATTTGTTGACAAATTCCTAGAAGACGTCAGAACTATATCATAGT	420
Qy	756	GAGGCTTTTACCGTTTAAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAAATTAATGATTAT	815
Db	421	GAGGCTTTTACCGTTTAAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAAATTAATGATTAT	480
Qy	816	GTTGAGAAAGGACCCAGGGTAAAGATCGTTCACCTAGTTAAAGAAATTAGATCGTGATACC	875
Db	481	GTTGAGAAAGGACCCAGGGTAAAGATCGTTCACCTAGTTAAAGAAATTAGATCGTGATACC	540
Qy	876	GTTCTCGCACTAGTTAACTATATTTTTTCAAGGGTAAAGTGGGAACGTCCTTTCCGAGGTT	935
Db	541	GTTCTCGCACTAGTTAACTATATTTTTTCAAGGGTAAAGTGGGAACGTCCTTTCCGAGGTT	600
Qy	936	AAAGTACTGAAGAGGAAGATTTTCATGTTGATCAAGTACTACTGTCAAGTTCCTCAAGT	995
Db	601	AAAGTACTGAAGAGGAAGATTTTCATGTTGATCAAGTACTACTGTCAAGTTCCTCAAGT	660
Qy	996	ATGAAAGACTGGGTATGTTTCAATATTTCAACATTTGCAAAATTAAGTTCCTGGGCTTTA	1055
Db	661	ATGAAAGACTGGGTATGTTTCAATATTTCAACATTTGCAAAATTAAGTTCCTGGGCTTTA	720
Qy	1056	TAAATGAAGTATTTAGGTAAAGCTGCTATTTTTTTTACCAGACGAAAGTAAAGCTT	1115
Db	721	TAAATGAAGTATTTAGGTAAAGCTGCTATTTTTTTTACCAGACGAAAGTAAAGCTT	780
Qy	1116	CAACATTTAGAGATGATGTTGACTCATGACATTTACTAAATTTTAGAGAACGAGGAT	1175
Db	781	CAACATTTAGAGATGATGTTGACTCATGACATTTACTAAATTTTAGAGAACGAGGAT	840
Qy	1176	CGTGTAGCGCTTCTCTGCACCTGCCAAAGTTAAGTATACCGGTACTTACGACTTAAA	1235
Db	841	CGTGTAGCGCTTCTCTGCACCTGCCAAAGTTAAGTATACCGGTACTTACGACTTAAA	900
Qy	1236	TCTGTTTGTAGCCAGTTAGGTATTTACCAAAAGTTTTTCTAACGGTCCCGATTGAGTGT	1295
Db	901	TCTGTTTGTAGCCAGTTAGGTATTTACCAAAAGTTTTTCTAACGGTCCCGATTGAGTGT	960
Qy	1296	GTTTACTGAAGAGCTCCATTAATAAATTTAGTAAAGCTGTTTCACAAAGCCGCTTAACTATT	1355
Db	961	GTTTACTGAAGAGCTCCATTAATAAATTTAGTAAAGCTGTTTCACAAAGCCGCTTAACTATT	1020
Qy	1356	GATGAAAGGTTACCGAGCGCGCGCGGTATGTTCTCGAAGCTATTTCCTGAGCATT	1415
Db	1021	GATGAAAGGTTACCGAGCGCGCGCGGTATGTTCTCGAAGCTATTTCCTGAGCATT	1080
Qy	1416	CCACCAAGCTTAAATTTAATAAACCATTGCTTTTTTCTGATGATCGAGCAGAACACTAAA	1475
Db	1081	CCACCAAGCTTAAATTTAATAAACCATTGCTTTTTTCTGATGATCGAGCAGAACACTAAA	1140
Qy	1476	AGCCCATGTTTATGGTAAAGTTGTCAACCCCAACTCAGAG 1517	
Db	1141	AGCCCATGTTTATGGTAAAGTTGTCAACCCCAACTCAGAG 1182	

RESULT 8
 AAV41730

Query Match 41.3%; Score 629.4; DB 19; Length 1260;
Best Local Similarity 70.8%; Pred. No. 3.2e-148;
Matches 837; Conservative 0; Mismatches 346; Indels 0; Gaps 0;

QY 1476 AGCCATTTGTTATGGTAAGTTGTCACCCCAACTCAGAAGT 1518
 DB 1216 AGCCCTCTTCATGGGAAGTGTGTCACCCCAAGCAGAAGT 1258

RESULT 9

AAQ89254
 ID AAQ89254 standard; cDNA; 1312 BP.

XX AAQ89254;
 AC XX
 XX 18-OCT-1995 (first entry)
 DT XX
 DE Human alpha-1-tryptsin cDNA.
 XX Alpha-1-tryptsin; protease-inhibitor; ss.
 KW XX
 XX Homo sapiens.

OS XX

XX Key Location/Qualifiers

FT CDS 28..1258

FT /*tag= a

FT sig_peptide 28..99

FT /*tag= b

FT mat_peptide 100..1255

FT /*tag= c

XX US5399684-A.

XX 21-MAR-1995.

XX 20-MAY-1982; 82US-0380310.

XX 20-MAY-1982; 82US-0380310.

XX 07-FEB-1984; 84US-0638980.

XX 03-MAR-1987; 87US-0022543.

XX 15-DEC-1987; 87US-0133190.

XX 16-SEP-1988; 88US-0246912.

XX 22-AUG-1989; 89US-0398288.

XX 11-MAR-1991; 91US-0666450.

XX 18-NOV-1992; 92US-0979556.

XX 02-JUL-1993; 93US-0086642.

XX (WASH-) WASHINGTON RES FOUND.

XX Davle EW, Kurachi K, Thirumalachary C, Woo SLC;

XX WPI; 1995-130740/17.

XX P-PSDB; AAR71969.

XX Human alpha-1-tryptsin (al-At) cDNA sequence - can be used for

XX the expression of al-At

XX Claim 1; Fig.1; 15pp; English.

XX The sequence of a human alpha-1-antitrypsin cDNA clone is given in

XX AAQ89254. Expression of the cDNA in host cell transformants has

XX allowed production of recombinant alpha-1-antitrypsin.

XX Sequence 1312 BP; 339 A; 368 C; 324 G; 281 T; 0 other;

XX Query Match 28.6%; Score 436.4; DB 16; Length 1312;

XX Best Local Similarity 59.8%; Pred. No. 1.1e-99;

XX Matches 731; Conservative 0; Mismatches 491; Indels 0; Gaps 0;

XX

QY 298 TGTGTGTAAGTCTCTGTTTCCCAAGTCAAGGCCATGGAAGCCCTCAAGCGCAGCGG 357

DB 62 TGGCAGCCCTGTGCTGCCTGCTCCCTGCTCCCTGGCTGAGGATCCCGAGGATGCTG 121

QY 358 CTCAAAACCGACACAGTCATCAGGACCAAGACCATCCGACTTTTAAATAAATTAATC 417

DB 122 CCAGAGAGACAGATACATACCCCATGATGATCAGGATCAGCCCAACCTTCAACAAGATCACC 181

QY 418 CAAATTTAGCCGAATTTGCTTTCTTCTTATAGACAATTAGCTCATCAAGTAATTTCTTA 477
 DB 182 CCAACTTGGCTGAGTTGGCTTACAGCCTATACCGCAGTGGCACACAGTCCCAACAGCA 241
 QY 478 CTAAACATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 537
 DB 242 CCAATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 301
 QY 538 CTAAGCCGATACCCATGACGAGATTTTGAAGGTTTAAACTTTTAACTTTTAACTTTTAACTTT 597
 DB 302 CCAAGGCTGACACTCACGATGAATCTTGGAGGCTTGAATTTCAACCTCACGAGATTC 361
 QY 598 CAGAAGCCCAATTTACGAGGTTTCTTCAAGAGTCTTCTCAGAACCTTTGGAATCAACTGAT 657
 DB 362 CGAGGCTCAGATCCATGAAGCTTCCAGGAACCTCTCCGTACCCCTCAACGAGCCAGACA 421
 QY 658 CTCATTTGCAATTAATACTTGTGTAACGGTTTATTTTCTCTGAAGTTTAAATTTGGTTG 717
 DB 422 GCAGCTCCAGCTGACCAACCGCAATGGCTTCTTCTCAGCGAGGCTTGAAGCTAGTGG 481
 QY 718 ACAAAATTTCTAGAAGACGCTCAAGAACTATATCATAGTAGGCTTTTACCGTTAAATTTG 777
 DB 482 ATAAGTTTGGAGGATGTTTAAAGTTGTACCACTCAGAAAGCTTCTCACTGTCAACTTCG 541
 QY 778 GTGATCTAGGAGCTAAAAGCAAAATTAATGATTTATTTGAGAAAGGACCCAGGTA 837
 DB 542 GGGACACCGAAGAGCCCAAGAACAGATCAACGATTAAGTGGAGAGGTTACTCAAGGA 601
 QY 838 AGATCGTTGACCTAGTTAAAGAAATTAGATCTGATACCGTCTTGGCACTAGTTAACTATA 897
 DB 602 AAATTTGGATTTGGTCAAGGAGCTTGACAGAGACACAGTTTTCCTCTCTGCTGAATTACA 661
 QY 898 TTTTTCACAGGTAAGTGGGAAGCTTCTTTCGAGGTTTAAAGTACTGAAGAGAGAGATT 957
 DB 662 TCTTCTTTAAAGGCAATGGGAGAGACCTTTTGAAGTCAAGGACACCGAGAGAGAGACT 721
 QY 958 TTCATGTTGATCAAGTTACTACTGTCAAAGTTCCAAATGATGAAGAACTGGGTATGTTC 1017
 DB 722 TCCAGTGGACAGGTGACCACTGCTGAAGTGGCTATGATGAAGCGTTTAGGCACTCTTA 781
 QY 1018 ATATTCAACATTTGCAAAATTAAGTTCTTGGGCTTATTAATGAAGTATTTAGGTAAAG 1077
 DB 782 ACATCCAGCATTTGAAGAGCTGCTCAGCTGGGTGCTGATGAATACCTGGGCAATG 841
 QY 1078 CTACTGCTATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1137
 DB 842 CCACCGCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 901
 QY 1138 CTCATGACATTTACTTAAATTTTGAAGAACGAGGATCGTGTAGCGCTTCTGTGACCC 1197
 DB 902 CCCAGATATCATCACCAGTTCTTGGAAATGAAGACAGAGGTTCTGCGAGCTTACATT 961
 QY 1198 TGCCAAAGTTAAGTATCACCAGTACTTACGACTTAAATCTGTTTTCGCGAGTTAGTGA 1257
 DB 962 TACCAAACTGTCATTTACTTGAACCTTATGATGAGAGCGTCTTGTAGTCAACTGAGGCA 1021
 QY 1258 TTACCAAAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1317
 DB 1022 TCATAAGGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1081
 QY 1318 AATTGAGTAAAGCTTTCACAAAGCGCTTAACTATTTGATCAAAAGGTTACCGAGGCGG 1377
 DB 1082 AGCTCTCCAGGCGGTGATAGGCTGCTGCTGACCATCGACGAGAAAGGAGTGAAGCTG 1141
 QY 1378 CCGGCGTATGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1437
 DB 1142 CTGGGCGCATGTTTTTAGAGGCAATACCCATGCTATCCGCCCCGAGGTCAAGTTCAACA 1201
 QY 1438 AACCAATTCGTTTTCTGATGATCGAGCAGAACACTAAAGGCCATTTGTTATGGGTAGG 1497
 DB 1202 AACCCCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1261

Mon Dec 9 12:50:56 2002

Db 1262 TGGTGAATCCACCACCAATA 1283

RESULT 12

AA545052 AAS45052 standard; cDNA; 1367 BP.

XX AC AAS45052;

XX DT 18-DEC-2001 (first entry)

XX DE cDNA encoding novel human secretory protein, Seq ID No 133.

XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen; ss.

XX OS Homo sapiens.

XX PN WO200166689-A2.

XX PD 13-SEP-2001.

XX PF 05-MAR-2001; 2001WO-US04942.

XX PR 07-MAR-2000; 2000US-0519705.

XX PR 19-MAY-2000; 2000US-0574454.

XX PR 17-JUN-2000; 2000US-0596193.

XX PR 14-JUL-2000; 2000US-0616847.

XX PR 19-SEP-2000; 2000US-0665363.

XX PR 20-OCT-2000; 2000US-0693267.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;

XX PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;

XX DR WPI: 2001-589934/66.

XX DR P-PSDB; AAU28152.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders - Claim 1; SEQ ID No 133; 107pp; English.

XX The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for

CC gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAS45052-AAS45295 represent novel human secreted protein coding sequences of the invention.

XX Sequence 1367 BP; 357 A; 392 C; 323 G; 295 T; 0 other;

XX Query Match 28.4%; Score 433.4; DB 22; Length 1367;

XX Best Local Similarity 60.2%; Pred. No. 6.1e-99;

XX Matches 736; Conservative 0; Mismatches 486; Indels 1; Gaps 1;

QY 298 TGTGTGTAAGTCTCTGTTTCCCACTCAAGCCATGGAAGACCTCAAGGCGAGCCG 357

DB 67 TGGCAGGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 126

QY 358 CTCAAAAACCGACACCATCATCACGACCAAGACCATCCGACTTTTATAAATTAATCT 417

DB 127 CCCAAGACAGATACATCCACCATGATCAGGATCACCAAGCTTCAACAGATCACCC 186

QY 418 CAAATTTAGCGGAATTTGCTTTTCTTTATAGACAAATAGCTCATCAAGTAATCTA 477

DB 187 CCAACCTGGCTGAGTGTGCTTTCAGCCCTATACCGCCAGGCGACACCATCCACAGCA 246

QY 478 CTACATTTTTTTTAGTCTCTTTTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 537

DB 247 CCAATATCTTCTCTCCAGTGAGCATCGTACAGCTTTGCAATGCTCTCCCTGGGA 306

QY 538 TAAAGCCGATACCCATGACGAGATTTTGAAGGTTTAACTTTAAATTTGACCAATCC 597

DB 307 CCAAGCTGACATCACGATGAATCTTGGAGGCGCTGAATTTCAACCTCAGGAGATC 366

QY 598 CAGAAGCCCAATTCACGAGGTTTTCAGAGAGTTGTTGAGAACTTTGAATCAACTGATT 657

DB 367 CGGAGGCTCAGATCCATGAAGCTTCCAGGACCTCTCCGTACCTCAACAGCAGACA 426

QY 658 CTCAATTTGCAATTAATCTGTAACGGTTTATTTTCTGTAAGGTTTAAATTTGTTG 717

DB 427 GCCAGCTCCAGCTGACACCGGCAATGGCTTCTCCTCAGCGAGGCGCTGAAGTAGTGG 486

QY 718 ACAATTTCTAGAACGCTCAGAACTATATCATAGTGAGGCTTTTACCGTTAATTTTG 777

DB 487 ATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCATCAGAACCTTCTACTGTCACTTCG 546

QY 778 GTGAT-ACGTGAGGAGCTAAAAAGCAAAATTAATGATTATGTTGAGAAAGGCCACCGGT 836

DB 547 GGGATCACCAGAGAGCCCAAGAACAGATCAACAGATTAGCTGGAGAGGGTACTCAAGGG 606

QY 837 AAGATCGTTGACCTAGTTTAAAGAAATAGATCGTGATACCGCTCTCGCACTAGTAACTAT 896

DB 607 AAAATTTGGATTTGGTCAAGGAGCTTGACAGAGACACAGTTTCTCTCTGGTGAATAC 666

QY 897 ATTTTTTCAAGGTAAGTGGGAACTGCTTTCGAGGTTTAAAGATACCTGAGAGGAGAT 956

DB 667 ATCTCTTTAAAGGCAAAATGGGAGACACCTTTTGAAGTCAAGGACACCGAGGACGAGGAC 726

QY 957 TTTCTATGTTGATCAAGTTACTACTGTCAAGTTTCCAAATGATGAAGACATGGGTATGTTTC 1016

DB 727 TTCACGTGACCGAGGTGACACCGTCCCTATGATGAAGCGTTTATGAGCATGTTT 786

QY 1017 AATATTCACATTCGCAAAATTAAGTTCTTGGTCTTATTAATGAAGTATTTAGGTAAC 1076

DB 787 AACATCAGCACTGTAAGAAAGCTGTCCAGCTGGTACTGCTATGAATACCTGGCAAT 846

QY 1077 GCTACTGCTATTTTTTTTTTACCAGAGCAAGGTAAGCTTCAACATTTAGAGAATGAGTTG 1136

RESULT 14

ABL67511	ABL67511 standard; DNA; 1352 BP.
ID	
XX	
AC	ABL67511;
XX	
DT	15-MAY-2002 (first entry)
XX	
DE	Thyroid cancer related gene sequence SEQ ID NO:5848.
XX	
KW	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW	gene; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200194629-A2.
XX	
PD	13-DEC-2001.
XX	
PF	30-MAY-2001; 2001WO-US10838.
XX	
PR	05-JUN-2000; 2000US-209473P.
PR	05-JUN-2000; 2000US-209531P.
PR	18-SEP-2000; 2000US-233133P.
PR	18-SEP-2000; 2000US-235617P.
PR	20-SEP-2000; 2000US-234009P.
PR	20-SEP-2000; 2000US-234034P.
PR	20-SEP-2000; 2000US-234052P.
PR	22-SEP-2000; 2000US-234509P.
PR	22-SEP-2000; 2000US-234567P.
PR	25-SEP-2000; 2000US-234923P.
PR	25-SEP-2000; 2000US-234924P.
PR	25-SEP-2000; 2000US-235077P.
PR	25-SEP-2000; 2000US-235082P.
PR	25-SEP-2000; 2000US-235134P.
PR	25-SEP-2000; 2000US-235280P.
PR	26-SEP-2000; 2000US-235637P.
PR	26-SEP-2000; 2000US-235638P.
PR	27-SEP-2000; 2000US-235711P.
PR	27-SEP-2000; 2000US-235720P.
PR	27-SEP-2000; 2000US-235840P.
PR	27-SEP-2000; 2000US-235863P.
PR	28-SEP-2000; 2000US-236028P.
PR	28-SEP-2000; 2000US-236032P.

```
Query Match      28.4%; Score 433.2; DB 24; Length 1352;
Best Local Similarity 59.7%; pred. No. 6.8e-99;
Matches 729; Conservative 0; Mismatches 493; Indels 0; Gaps 0;
```

298	QY	TGTTGTGGTAAGTCCTGTGTTTTCCCGCAGTCAAGGCCATCGAAGACCCCTCAAGCGCACGCCG	357
54	Dd	TGGCAGGCCTGTGCTGGCCTGTGCTCCCTGTCTCCCTGGCTGAGGATCCCCGAGGAGATGCTG	113
358	QY	CTCAAAAACCCAGACCAGCATCATCAGCACCAAGACCATCCGACTTTTAAATAAAATTACT	417
114	Dd	CCCAGAAGACAGATACATCCCACCATGATCAGGATCACCCAACCTTCAACAAGATCACCC	173
418	QY	CRAATTTTAGCGAAATTTGCTTTTCTTTTGATATAGACAATTAGCTCATCAAAGTAATTTCTA	477
174	Dd	CCAACTGGCTGAGTTCGCTTCAGCCTATACCGCCGAGCTGGCACACCAAGTCCAACGCA	233
478	QY	CTAACATTTTTTTTAGTCTCTGTTTCTATTGGCCACTGCTTTGCCCATGTTGAGTTTAGGTA	537
234	Dd	CCAATATCTTCTCTCCCGAGTGAGCATCGCTACAGCCCTTTTGCATGCTGCTCCCTGGGA	293

ftp.wipo.int/pub/published_pct_sequences.

XX sequence 1371 BP: 350 A: 388 C: 340 G: 293 T: 0 other;
 SO

Query Match	28.4%	Score 433.2	DB 24	Length 1371

Query Match	28.4%	Score 43.27	22.2%
Best Local Similarity	59.78%	Pred. No. 6.8e-99;	

BEST LOCAL SIMILARITY	55.76;	Exact matches	0;
Matches	729;	Conservative	0;
		Mismatches	493;
		Indels	0;
		Gaps	0;

208 TCTCTCCTAAGTCCTGTGTTTCCCAAGTCAAGGCCATGGAAGACCCCTCAAGGCCAGCCG 357

QY
298 TGGTGGTAAGTCCTGIGTTCCCAATCAGGCCCATCGAAGCCCATACGACGCGGTCT

73 TGGCAGGCCTGTGCTGCCTGGTCCCTGCTCCCTGGCTGAGGATCCCAGGGAGATGCTG 132

[illegible]

QV 358 CTCAAAAACCGACACCAAGTCATCAGGACCAAGACCTTTAATAAATTAATC 417

192

D_b 133 CCCAGAAGACAGATACATCCACCATGATCAGGATCACCCCAACCTTCAACAAGATCACCC 192

477

QY
418 CAAATTTAGCCGAATTGCTTTCCTTGTAAGACCAATAGCCCATCCTGCTTTC

193 CCAACCTGGCTGAGTTCGCCCTTCAGCCTATACCGCCAGCTGGCACACAGTCCAACAGCA 252

[illegible]

QY 478 CTAACATTTTTTTAGTCCTGTTTCTATTGCCACTGCTTTCGCCATGTTGAGTTAGGTA 537

7

Db 253 CCAATATCTTCTCTCCCCAGTGAGCATCGCTACAGCCCTTTGCAAATGCTCTCTCCCTGGGGA 312

597 TCCGAAATTCATTAGAGGTTAACCTTAACTTGACCGAAATCC

QY
538 C T A A G C C G A T A C C C A T G A C G A G A I I T A G A A G N I I T A F A C I I T A T I T G C C C C T T T C

313 CCAAGGCTGACACTCACGATGAAATCCTGGAGGCCCTGAATTCAACCTCACGGAGATTC 372

[illegible]

QY 598 CAGAAGCCCCAAATTCACGAGGGTTTCAAGAGTTGTTGAGAACTTTGAATCAACCTGATT 657

432

Db 373 CGGAGGCTCAGATCCATGAAGGCTTCCAGGAATCCCTCCGTACCTCTCAACCGAGCCAGACG 452

658 CTCATTTCCAAATTAACTACTGGTAACGGTTATTTTGTCTGAAGGTTTAAATTTGGTTG 717

[illegible]

Db 433 GCCAGCTCCAGCTGACCAACCGCAATGGCCGTTCCTCAGCGAGGCCCTGAAGCTAGTGG 492

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

QY 718 ACAAATTCCTAGAAGACGTCAGAACTATATCATAGTGAGGCTTTACCGTTAATTGG 777

552

D6 493 ATAAAGTTTGGAGGA'G'T'AAAAAGTTGTACCACTCAGAAGCCTTCACCTGCACACAC

778 CTGATACCTGAGGAAGCTAAAAGCAAAATTAAATGATTATGTTGAGAAAGGCACCCAGGTA 837

[illegible]

Db 553 GGGACACCGAAGAGGCCCAAGAAACAGATCAACGATTACGTGGAGAAGGTTACTCAAGGGA 612

907 E. CECILIA ST. #100

QY 838 AGATCGTTGACCTAGTTAAAGAAATTAGATCGTGGATACCGTCTTCGCACTAGTTAACATA 89

•